



## SEQUENCE LISTING

<120> Matsui, Toshimitsu  
Aaronson, Stuart H.  
Pierce, Jacalyn H.

<120> TYPE ALPHA PLATELET DERIVED GROWTH  
FACTOR RECEPTOR

<130> 14014.0279US

<140> 08/439,095  
<141> 1995-05-11

<150> 07/915,884  
<151> 1992-07-20

<150> 07/308,282  
<151> 1989-02-09

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1089  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 1  
Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr  
1 5 10 15  
Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro  
20 25 30  
Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg  
35 40 45  
Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu  
50 55 60  
Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Asn Asn Ser Gly Leu  
65 70 75 80  
Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly  
85 90 95  
Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu  
100 105 110  
Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe  
115 120 125  
Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp  
130 135 140  
Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr  
145 150 155 160  
Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln  
165 170 175  
Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr  
180 185 190  
Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu  
195 200 205

Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val  
 210 215 220  
 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn  
 225 230 235 240  
 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys  
 245 250 255  
 Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val  
 260 265 270  
 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr  
 275 280 285  
 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys  
 290 295 300  
 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr  
 305 310 315 320  
 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val  
 325 330 335  
 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn  
 340 345 350  
 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu  
 355 360 365  
 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala  
 370 375 380  
 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp  
 385 390 395 400  
 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser  
 405 410 415  
 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr  
 420 425 430  
 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met  
 435 440 445  
 Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile  
 450 455 460  
 Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp  
 465 470 475 480  
 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr  
 485 490 495  
 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg  
 500 505 510  
 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala  
 515 520 525  
 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val  
 530 535 540  
 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg  
 545 550 555 560  
 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp  
 565 570 575  
 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly  
 580 585 590  
 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val  
 595 600 605  
 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val  
 610 615 620  
 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala  
 625 630 635 640  
 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn  
 645 650 655  
 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile  
 660 665 670  
 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys  
 675 680 685

Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu  
 690 695 700  
 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr  
 705 710 715 720  
 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln  
 725 730 735  
 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser  
 740 745 750  
 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr  
 755 760 765  
 Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp  
 770 775 780  
 Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr Tyr  
 785 790 795 800  
 Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His  
 805 810 815  
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val  
 820 825 830  
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn  
 835 840 845  
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro  
 850 855 860  
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser  
 865 870 875 880  
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr  
 885 890 895  
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly  
 900 905 910  
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile  
 915 920 925  
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr  
 930 935 940  
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys  
 945 950 955 960  
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala  
 965 970 975  
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr  
 980 985 990  
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp  
 995 1000 1005  
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp  
 1010 1015 1020  
 Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn Arg His  
 1025 1030 1035 1040  
 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser  
 1045 1050 1055  
 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met  
 1060 1065 1070  
 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe  
 1075 1080 1085  
 Leu

<210> 2  
 <211> 6413  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 Synthetic Construct

<400> 2

ccattactgt	tggagctaca	gggagagaaa	caggaggaga	atgcaagaga	tcatttggga	60
aggccgtggg	cacgccttt	actccatgt	tggacattc	attgcgaaat	aacatcgag	120
gagaagtttcc	ccagagctat	ggggacttcc	catccggcgt	tcctggctt	aggctgtctt	180
ctcacagggc	tgagccta	cctctgcag	cttcatc	cctctatcct	tccaaatgaa	240
aatgaaaagg	ttgtgcagct	gaattcatcc	tttctctga	gatgcttgg	ggagagtgaa	300
gtgagctggc	agtacccat	gtctgaagaa	gagagctccg	atgtggaaat	cagaaatgaa	360
gaaaacaaca	gcggcctttt	tgtgacggtc	ttgaaagtga	gcagtgcctc	ggcgccccac	420
acagggttgt	acacttgcta	ttacaaccac	actcagacag	aagagaatga	gcttgaaggc	480
aggcacattt	acatctatgt	gccagacca	gatgttagcct	ttgtacctct	aggaatgacg	540
gattattnag	tcatctgtt	ggatgtat	tctgcattt	taccttgc	cacaactgat	600
cccgagactc	ctgttaacctt	acacaacagt	gaggggttgg	tacctgcctc	ctacgacagc	660
agacagggtt	ttaatggac	tttcaactgt	ggcccata	tctgtgaggc	caccgtcaaa	720
ggaaaagaagt	tccagaccat	cccatttaat	gttatgtctt	taaaagcaac	atcagagctg	780
gatctagaaaa	tggaaagctct	taaaaccgt	tataagtca	gggaaacat	tgtggtcacc	840
tgtgctgttt	ttaacaatga	ggtgggttgc	cttcaatgga	cttaccctgg	agaagtgaaa	900
ggcaaaggc	tcacaatgct	ggaagaaatc	aaagtccat	ccatcaaatt	ggtgtacact	960
ttgacggtcc	ccgaggccac	ggtgaaagac	agtggagatt	acgaatgtc	tgcccgccag	1020
gctaccagg	aggtcaaaaga	aatgaagaaa	gtcaactattt	ctgtccatga	gaaagggttc	1080
attgaaatca	aaccaccc	cagccagg	gaagctgtca	acctgcatt	agtcaacat	1140
tttgtttag	aggtgcgggc	ctaccac	cccaggat	cctggctgaa	aaacaatctg	1200
actctgattt	aaaatctc	tgagatcacc	actgatgtgg	aaaagattca	ggaaataagg	1260
tatcgaagca	aattaaagct	gatccgt	aagaagaag	acagtggcca	ttatactatt	1320
gtagctcaaa	atgaagatgc	tgtgaagagc	tatactttt	aactgttac	tcaagttcct	1380
tcatccattt	tggacttgg	cgatgatc	catggctca	ctggggaca	gacggtgagg	1440
tgcacagct	aaggcacg	gcttcctgat	attgagtgg	tgatatgca	agatattaag	1500
aaatgtata	atgaaactt	tgggactt	ttggcaaca	atgtctca	catcatc	1560
gagatccact	cccgagacag	gagtgccgt	gagggccgt	tgactttc	caaagtggag	1620
gagaccatcg	ccgtgcgt	cctggctca	aatctcctt	gagctgagaa	ccgagagctg	1680
aagctgg	ctcccac	gcgttctgaa	ctcacgg	ctgctgc	cctggctg	1740
tttgttattt	tgatcatc	acttatttgc	ctgggttgc	tttggaaaca	gaaaccgagg	1800
tatgaaattt	gctggagg	cattgaatca	atcagccc	atggacat	atataattat	1860
gtggacccg	tgcaactg	ttatgact	agatggag	ttccaagaga	ttgacttagt	1920
cttggcgg	tcttgggt	tggagcgtt	gggaggtgg	ttgaagga	agcctatg	1980
ttaagccg	cccaac	catgaaat	gcgtgaaga	tgctaaaacc	cacggccaga	2040
tccagtgaaa	aacaagct	catgtctg	ctgaagata	tgactcac	ggggccacat	2100
ttgaacattt	taaacttgc	gggagcctg	accagg	gccccattt	catcatcaca	2160
gagtatttgc	tctatgg	tttggtca	tattgcata	agaatagg	tagttcct	2220
agccaccacc	cagagaagcc	aaagaaag	ctggat	ttggattgaa	ccctgctg	2280
gaaagcacac	ggagctat	tattttat	tttggaaaca	atggtact	catggacat	2340
aagcaggct	atactacaca	gtatgtccc	atgtggat	ggaaagg	ttctaaat	2400
tccgacatcc	agagatact	ctatgat	ccagcct	ataagaagaa	atctatgt	2460
gactcagaag	tcaaaaac	ccttc	catgat	aaggc	tttatttgg	2520
tttgtttag	tcacca	agttggcc	ggaatgg	tttggctt	aaaaattt	2580
gtccaccgt	atctgg	tcgcaac	ctc	aggaaat	tgtgaagat	2640
tgtgactt	gcctggcc	agacat	catgat	ttgac	tttggatcc	2700
accttct	ccgt	gatgg	gagacat	tttgg	tttggatcc	2760
ctgagtgt	tctgtt	tgg	tttgg	tttgg	tttggatcc	2820
ccttaccc	gcat	ggatt	tttacaata	atgtca	tttggatcc	2880
atggcca	ctgacc	tacc	gttac	tttgg	tttggatcc	2940
agtgagcc	agaagag	gttac	tttgg	tttgg	tttggatcc	3000
cctggaca	ataaaaag	ttatgaaaa	attc	tttgg	tttggatcc	3060
cctgtgt	cacg	tttgg	tttgg	tttgg	tttggatcc	3120
aacgag	acaag	ggact	tttgg	tttgg	tttggatcc	3180
gacagt	acat	gggtt	tttgg	tttgg	tttggatcc	3240
ggcaag	acag	tttgg	tttgg	tttgg	tttggatcc	3300
agcagt	cc	tttgg	tttgg	tttgg	tttggatcc	3360
gacatcg	tagact	tttgg	tttgg	tttgg	tttggatcc	3420
aggggtt	tccact	tttgg	tttgg	tttgg	tttggatcc	3480
aatgcgg	tttgg	tttgg	tttgg	tttgg	tttggatcc	3540

ctcggggagc gttctaaata tgaatgaatg ggatatttg aaatgaactt tgtcagtgtt	3600
gcctctcgca atgcctcagt agcatctcag tgggtgtgtga agtttggaga tagatggata	3660
agggataaat aggccacaga aggtgaacct ttgtcttcaa ggacattgg tagaggtccaa	3720
cagacacaat ttatactgcg acagaacctc agcattgtaa ttatgtaaat aactctaacc	3780
aaggctgtgt ttagattgtta tttaactatct tctttggact tctgaagaga ccactcaatc	3840
catccatgtt ctccctctt gaaacctgtat gtcaagctgt gttgaacttt ttaaagaagt	3900
gcatgaaaaa ccattttga accttaaaaag gtactggat tatagoattt tgctatctt	3960
tttagtgtta aagagataaa gaataataat taaccaaccc ttttaatag atttgggtca	4020
tttagaagcc tgacaactca ttttcatatt gtaatctatg ttataatac tactactgtt	4080
atcagaatgt ctaaatgtgt aataatgtaa catgatttcc ctccagagaa agcacaattt	4140
aaaacaatcc ttactaagta ggtgatgagt ttgacagttt ttgacattt tattaaataa	4200
catgttctc tataaagtat ggtaatagct ttagtgaatt aaatttagtt gagcatagag	4260
aacaaagtaa aagttagtgtt gtccaggaag tcagaatttt taactgtact gaataggttc	4320
cccaatccat cgtattaaaa aacaattaac tgccctctga aataatggaa ttagaaacaa	4380
acaaaactct taagtcctaa aagttctcaa tggtagaggca taaacctgtg ctgaacataa	4440
cttctcatgt atattaccca atggaaaata taatgatcag caaaaagact ggatttgcag	4500
aagttttttt ttttttctt catgcctgtat gaaagctttg gcaaccccaa tatatgtatt	4560
ttttgaatct atgaacctga aaagggtcag aagatgccc agacatcagc ctccctctt	4620
caccccttac cccaaagaga aagagttga aactcgagac cataaagata ttcttttagtg	4680
gaggctggat gtgcatttgc ctggatcctc agttctcaa ttgtgtgtgc agccaggatg	4740
actagatccct gggttccat ctttgcattt ctgaagtatg aagtctgagg gaaaccagag	4800
tctgtatccc tctaaactcc ctggcttgc tgatcgccca gtttccgaa acactgactt	4860
aggtttcagg aagttgccat gggaaacaaa taatttgaac ttggAACAG ggttggaaatt	4920
caaccacgc ggaagcctac tatttaaattt cttggcttca ggttagtgc atttaatgcc	4980
atctagcttag caattgcgac cttaaattttt cttccagtc tttagctgagg ctgagaaagc	5040
taaagttgg ttttgcagg ttttccaaaa gtaaagatgc tacttcccac tttatggggg	5100
agattgaact ttccccgtct cccgtcttgc gcctccact ccatacccg ccaagggaaag	5160
gcatgtacaa aaattatgc attcgtgtt ccaagtctct gtgttaaccag ctcagtgtt	5220
tggtgaaaaa aacattttaa gtttactgtatgaaatgggatggatggaa ggtgaatttgc	5280
tcacatctat ccacactgtc aaacagggtt gtgtgggttc attggcattt tttcaatac	5340
tgcttaattt ctgataccat atgaatggaa catggctgtt gattactgc attactgtgc	5400
tatcggcaga tgatgttttgc gaagatgcgaa aagcaataat aaagtacttgc actacctact	5460
ggtgtaatct caatgcgac cccaaacttcc ttatccaact tttcatatgt aagtgcgaaag	5520
actgagccag attggccaaat taaaacggaa aactgtacta ggttctgttag agccaatttgc	5580
acttgaataa cgttttgtt tcttagatca cagctcaaggc attctgtttt tcgctcactc	5640
tcccttgcac agccttattt tgggtgtgtt ttgcatttttgc atattgtgtt gggcttgc	5700
tgacatcatg aggccggatg aaacttctca gtccagcgtt ccaggatctt aacaaatgt	5760
cccacctgaa ttttatatg actgcatttgc tgggtgtgtt gttgtttca gcaaaatttca	5820
gatttttttcc ttttggcct cctgcacaaatg ctccagaaga aaatttgcctt atctttccta	5880
ctttcttattt ttatgtatgc aatcaaagcc ggcttgcggaa acactatttgc tgacttttgc	5940
aacgattatgt gatgccttta aatgtggc tgccaaatctg tacaaaatgg tcctattttgc	6000
gtgaagaggg acataagata aatgtatgtt atacatcaat atgtatatat gtatttttat	6060
atagacttgg agaataactgc caaaacattt atgacaagct gtatcactgc ctgcgtttat	6120
atttttttaa ctgtgataat ccccacaggc acattaacttgc ttgcacttttgc gaaatgtccaa	6180
aatttatatt tttagaaataa taaaagaaaa gataacttaca tggccaaaa acaatgggt	6240
ggtaatgtt tgagaaaaac taacttgcata gggcttacca atacaaaatgt tattacgaat	6300
ccccctgttc atgttttgc tttaaaacgt gtaaatgttgc atctttatat ttcaataataat	6360
gatataataat tttaaagttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaaaa aaa	6413